

Please amend the following claims:

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2. (Amended) The method of claim 1 in which the genome of the wild strain of *Shigella* is modified, wherein both [so that] a ~~first gene~~ or genes, coding for a protein or proteins necessary for the wild strain of *Shigella* to invade cells, as well as tissues, of the host, and a second gene or genes, coding for a protein or proteins necessary for the wild strain of *Shigella* to spread within infected cells and between infected and uninfected cells of the host, are wholly or partly removed or permanently inactivated.

Claim 3, line 2, after "first gene" insert ~~insert~~ --or genes--.

Claim 4, line 2, delete "intra-intercellular" and insert therefor ~~for~~ -- intra- or intercellular--.

Claim 6, line 1, after "first gene" insert ~~insert~~ --or genes--.

Claim 7, line 2, delete "intra-intercellular" and insert therefor ~~for~~ -- intra- or intercellular--.

Claim 8, line 1, after "first gene" insert ~~insert~~ or genes--.

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10. (Amended) The method of claim 2 in which one or more of the genes are inactivated by allelic exchange with one or more [*in vitro*] mutagenized genes, wherein said mutagenized genes have been mutagenized in vitro [especially mutagenized genes from which significant portions have been deleted and particularly mutagenized genes into which marker genes have been inserted].

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13. (Amended) A *Shigella* comprising an inactivated *Shiga*-toxin gene, other than ~~only~~ by inactivation by means of a transposon inserted into the gene, and wherein said *Shigella* is other than those designated SC501, SC504, SC505, and SC506.

Please add the following new claims:

--15. The method of claim 10, wherein said mutagenized genes are mutagenized genes from which nucleotide sequences have been ~~deleted~~.

16. The method of claim 10, wherein said mutagenized genes are mutagenized genes into which marker genes have been inserted.

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17. A modified, wild strain of an enteroinvasive *Shigella* that can be used for making a vaccine against the wild strain of *Shigella*, wherein the genome of the wild strain of *Shigella* has been transformed, other than only by inactivation by means of a transposon inserted into genes of the genome, so that it cannot substantially invade cells of a host, and cannot spread substantially within infected cells and from infected to uninfected cells of the host, and cannot produce toxins that will kill substantial numbers of the host's infected, as well as uninfected, cells, wherein the modified wild strain is selected from the group consisting of:

(A) a wild strain of *Shigella*, the genome of which is modified so that a first gene, coding for a protein necessary for the wild strain of *Shigella* to invade cells, as well as tissues, of the host, and a second gene, coding for a protein necessary for the wild strain of *Shigella* to spread within infected cells and

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between infected and uninfected cells of the host, are wholly or partly removed or permanently inactivated, wherein the *Shigella* is an *S. flexneri* and the first gene codes for the production or use of aerobactin by the *S. flexneri* and the second gene codes for intra- or intercellular spread; and

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(B) a wild strain of *Shigella*, the genome of which is modified so that a first gene, coding for a protein necessary for the wild strain of *Shigella* to invade cells, as well as tissues, of the host, and a second gene, coding for a protein necessary for the wild strain of *Shigella* to spread within infected cells and between infected and uninfected cells of the host, are wholly or partly removed or permanently inactivated, in which the *Shigella* is an *S. dysenteriae* 1, the genome of which is modified so that a third gene, coding for the production or use of *Shiga*-toxin by the *S. dysenteriae* 1, is wholly or partly removed or permanently inactivated; and

(C) a *Shigella* comprising an inactivated *Shiga*-toxin gene.

18. The modified wild strain of enteroinvasive *Shigella* of claim 17, wherein the first gene of the *S. dysenteriae* 1 codes for the production or use of enterochelin by the *S. dysenteriae*

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